

cacgaggaacaacctctctctcscagcagagagtgtcacctcctgctttaggaccatcaagctctgctaactgaatc -474
 tcatacctaattgcaggatcacattgcaaagctttcactctttcccaccttgcttgtgggtaaatctcttctgcggaatc -395
 tcagaaagtaaagttccatcctgagaatatttcacaaagaatttccttaagagctggactgggtcttgacccttggaat -316
 ttaagaaattcttaagacaatgtcaaataatgatccaagagaaaatgtgatttgagctctggagacaattgtgcatatcg -237
 tctaataataaaaaccatactagcctatagaaaacaatatttgaataataaaaaccatactagcctatagaaaacaa -158
 tatttgaaagattgctaccactaaaaagaaaactactacaacttgacaagactgctgcaaacttcaattgggcaccaca -79
 acttgacaagggtgctataaaacaagattgctacaacttctagtttatgtttatacagcatatttcatttgggcttaatg -1

atg gag aaa aag tgt acc ctg tat ttt ctg gtt ctc ttg cct ttt ttt atg att ctt gtt
 1 M E K K C T L Y F L V L L P F F M I L V 60
 aca gca gaa tta gaa gag agt cct gag gac tca att cag ttg gga gtt act aga aat aaa
 21 T A E L E E S P E D S I Q L G V T R N K 120
 atc atg aca gct caa tat gaa tgt tac caa aag att atg caa gac ccc att caa caa gca
 41 I M T A Q Y E C Y Q K I M Q D P I Q Q A 180
 gaa ggc gtt tac tgc aac aga acc tgg gat gga tgg ctc tgc tgg aac gat gtt gca gca
 61 E G V Y C N R T W D G W L C W N D V A A 240
 gga act gaa tca atg cag ctc tgc cct gat tac ttt cag gac ttt gat cca tca gaa aaa
 81 G T E S M Q L C P D Y F Q D F D P S E K 300
 gtt aca aag atc tgt gac caa gat gga aac tgg ttt aga cat cca gca agc aac aga aca
 101 V T K I C D Q D G N W F R H P A S N R T 360
 tgg aca aat tat acc cag tgt aat gtt aac acc cac gag aaa gtg aag act gca cta aat
 121 W T N Y T Q C N V N T H E K V K T A L N 420
 ttg ttt tac ctg acc ata att gga cac gga ttg tct att gca tca ctg ctt atc tcg ctt
 141 L F Y L T I I G H G L S I A S L L I S L 480
 ggc ata ttc ttt tat ttc aag agc cta agt tgc caa agg att acc tta cac aaa aat ctg
 161 G I F F Y F K S L S C Q R I T L H K N L 540
 ttc ttc tca ttt gtt tgt aac tct gtt gta aca atc att cac ctc act gca gtg gcc aac
 181 F F S F V C N S V V T I I H L T A V A N 600
 aac cag gcc tta gta gcc aca aat cct gtt agt tgc aaa gtg tcc cag ttc att cat ctt
 201 N Q A L V A T N P V S C K V S Q F I H L 660
 tac ctg atg ggc tgt aat tac ttt tgg atg ctc tgt gaa ggc att tac cta cac aca ctc
 221 Y L M G C N Y F W M L C E G I Y L H T L 720
 att gtg gtg gcc gtg ttt gca gag aag caa cat tta atg tgg tat tat ttt ctt ggc tgg
 241 I V V A V F A E K Q H L M W Y Y F L G W 780
 gga ttt cca ctg att cct gct tgt ata cat gcc att gct aga agc tta tat tac aat gac
 261 G F P L I P A C I H A I A R S L Y Y N D 840
 aat tgc tgg atc agt tct gat acc cat ctc ctc tac att atc cat ggc cca att tgt gct
 281 N C W I S S D T H L L Y I I H G P I C A 900
 gct tta ctg gtg aat ctt ttt ttc ttg tta aat att gta cgc gtt ctc atc acc aag tta
 300 A L L V N L F F L L N I V R V L I T K L 960
 aaa gtt aca cac caa gcg gaa tcc aat ctg tac atg aaa gct gtg aga gct act ctt atc
 321 K V T H Q A E S N L Y M K A V R A T L I 1020

FIG. 1A

ttg gtg cca ttg ctt ggc att gaa ttt gtg ctg att cca tgg cga cct gaa gga aag att
 341 L V P L L G I E F V L I P W R P E G K I 1080
 gca gag gag gta tat gac tac atc atg cac atc ctt atg cac ttc cag ggt ctt ttg gtc
 381 A E E V Y D Y I M H I L M H F Q G L L V 1140
 tct acc att ttc tgc ttc ttt aat gga gag gtt caa gca att ctg aga aga aac tgg aat
 401 S T I F C F F N G E V Q A I L R R N W N 1200
 caa tac aaa atc caa ttt gga aac agc ttt tcc aac tca gaa gct ctt cgt agt gcg tct
 421 Q Y K I Q F G N S F S N S E A L R S A S 1260
 tac aca gtg tca aca atc agt gat ggt cca ggt tat agt cat gac tgt cct agt gaa cac
 441 Y T V S T I S D G P G Y S H D C P S E H 1320
 tta aat gga aaa agc atc cat gat att gaa aat gtt ctc tta aaa cca gaa aat tta tat
 462 L N G K S I H D I E N V L L K P E N L Y 1380
 aat tga aaatagaaggatggttgtctcactgtttggtgcttctcctaactcaaggacttggacccatgactctgtag
 N
 ccagaagacttcaatattaaatgactttggggaatgtcataaagaagagccttcacatgaaattagtagtgtgttgata 1536
 agagtgtaacatccagctctatgtgggaaaaaagaaatcctgggttgtaatgtttgtcagtaaatactcccactatgcc 1615
 tgatgtgacgctactaacctgacatcaccaagtgtggaattggagaaaagcacaatcaacttttctgagctggtgtaag 1694
 ccagttccagcacaccattgatgaattcaaacaatggctgtaaaactaaacatacatgttgggcatgattctaccctt 1773
 attcscaccaagagacctagctaaggtctataaacatgaagggaattagcttttagttttaaaactctttatcccat 1852
 cttgattggggcagttgactttttttttttccagagtgccgtagtcctttttgttaactaccctctcaaatggacaata 1931
 ccagaagtgaattatccctgctggcctttcttttctctatgaaaagcaactgagtacaattgttatgatctactcatttg 2010
 ctgacacatcagttatatcttgtggcatatccattgttgaaactggatgaacaggatgtataatatgcaatcttacttc 2089
 tatatcattaggaacacatcttagttgatgtacaaaacaccttgtcaacctcttctgtcttaccacacagtgggagg 2168
 gaattcctagctgtaaatataaattttgcccttccatttctactgtataaacaattagcaatcattttatataaagaa 2247
 aatcaatgaaggatttcttatttttcttgggaattttgtaaaaaagaaattgtgaaaaatgagcttgtaaatactccattat 2326
 tttattttatagtctcaaatcaatacacatacacctatgtaatttttaagcaaatatataatgcaacaatgtgtgtat 2405
 gttaatatctgatactgtatctgggctgatttttttaataaaatagagtctggaatgctaaaaaaaaaaaaaaaaa 2481

FIG. 1B

HPhobic HPhilic

Hydropathy Plot of the Human CGRP Receptor Peptide Sequence

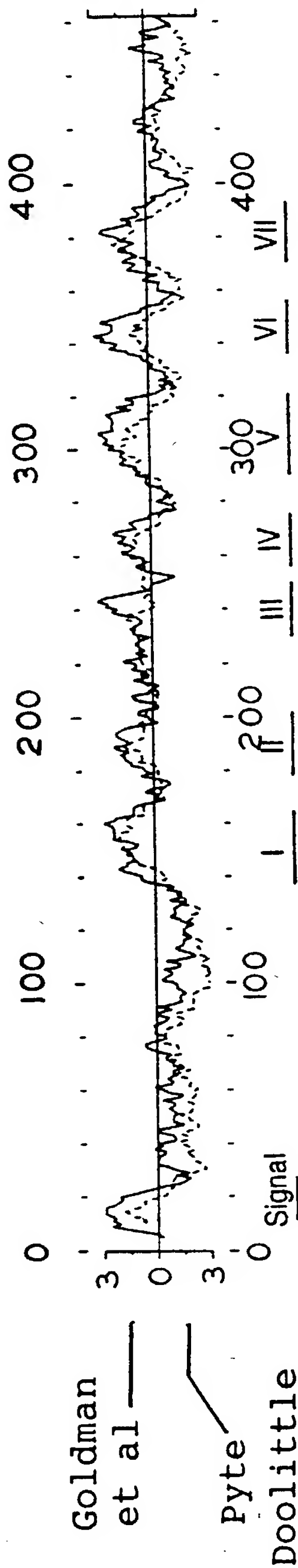


FIG. 2

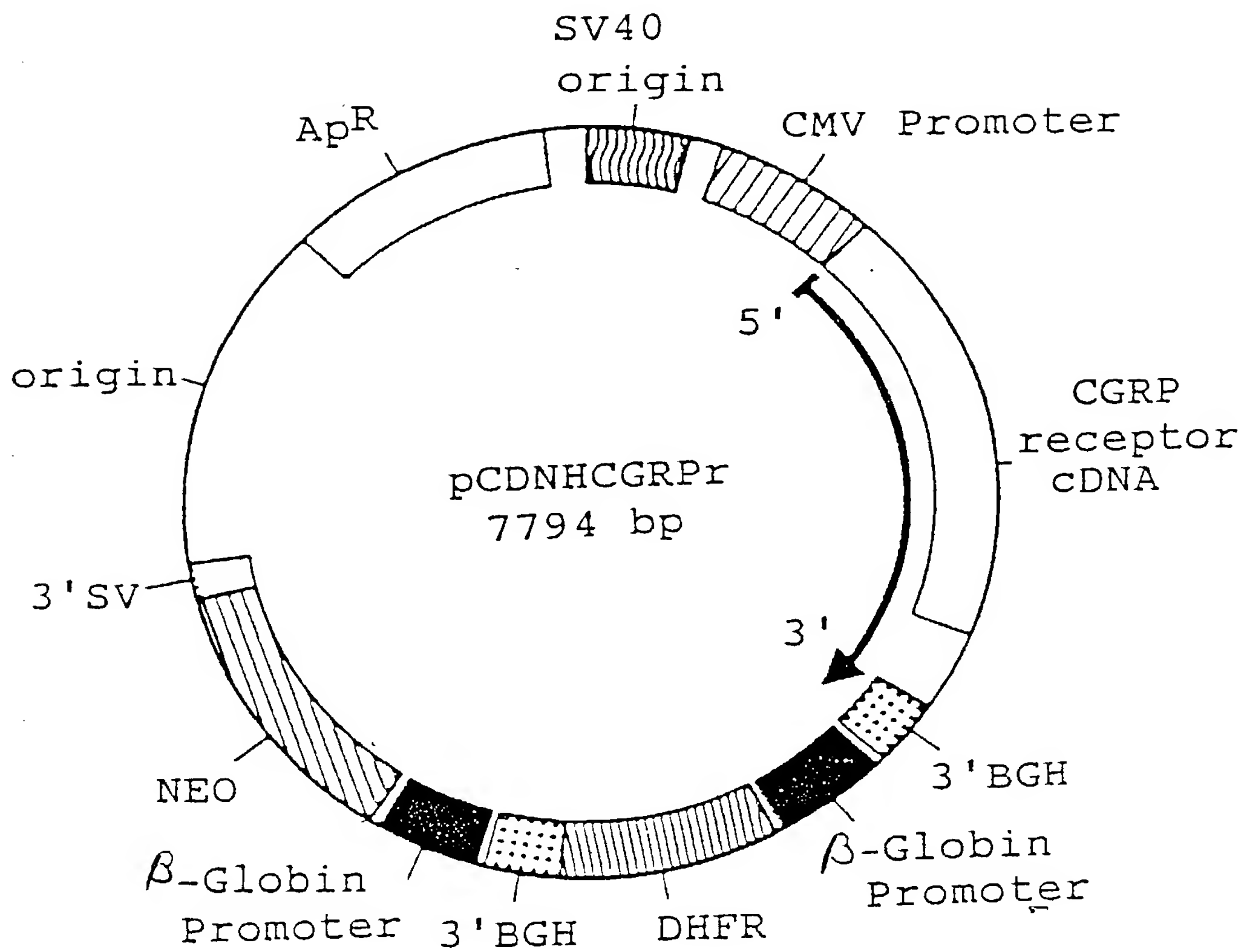


FIG. 4

CAMP RESPONSE IN 293 CELLS

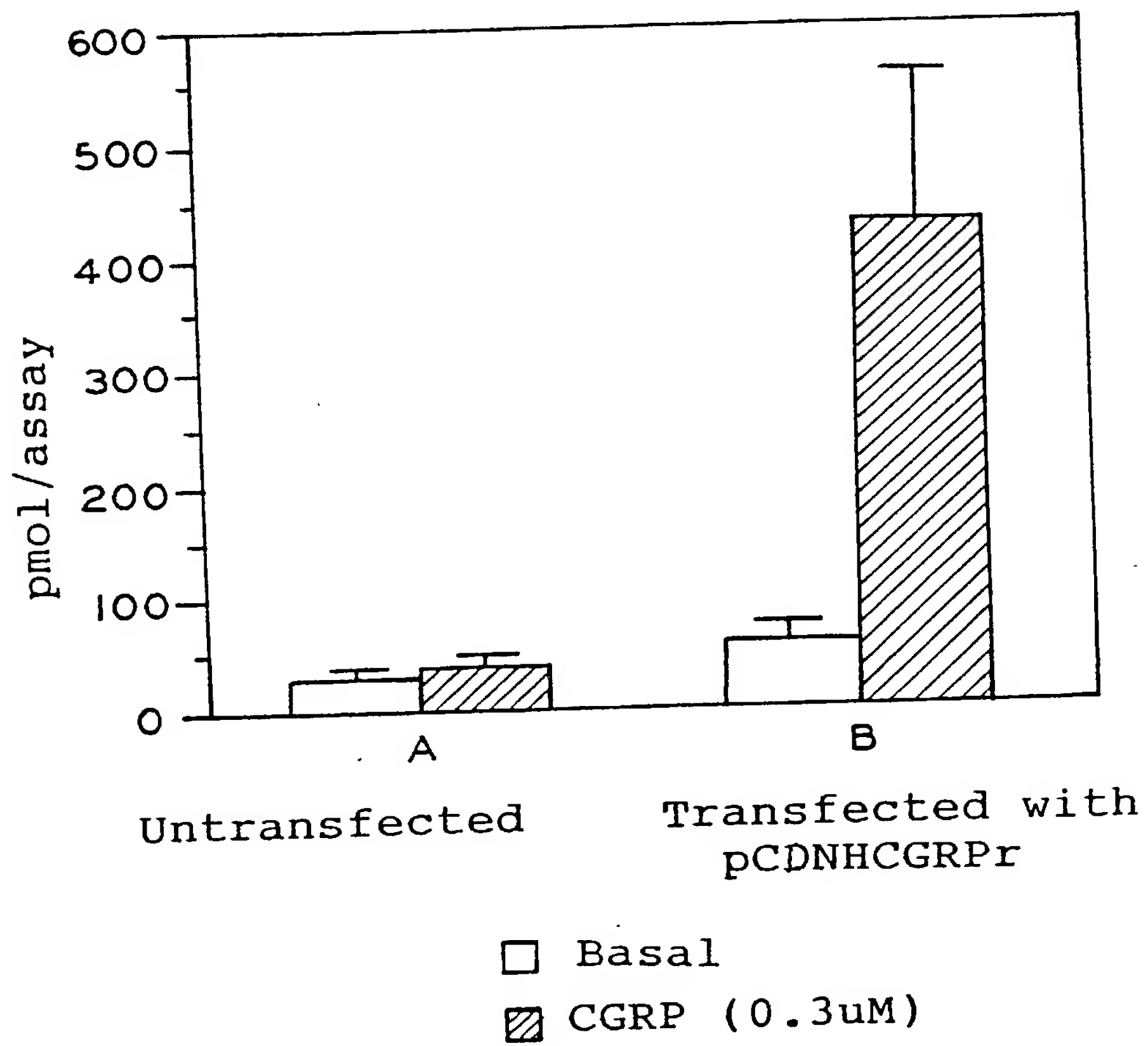


FIG. 5

EFFECT OF CGRP TREATMENT OF 293
CELL LINES STABLY TRANSFORMED
WITH THE pCDNHCGRP α CONSTRUCT

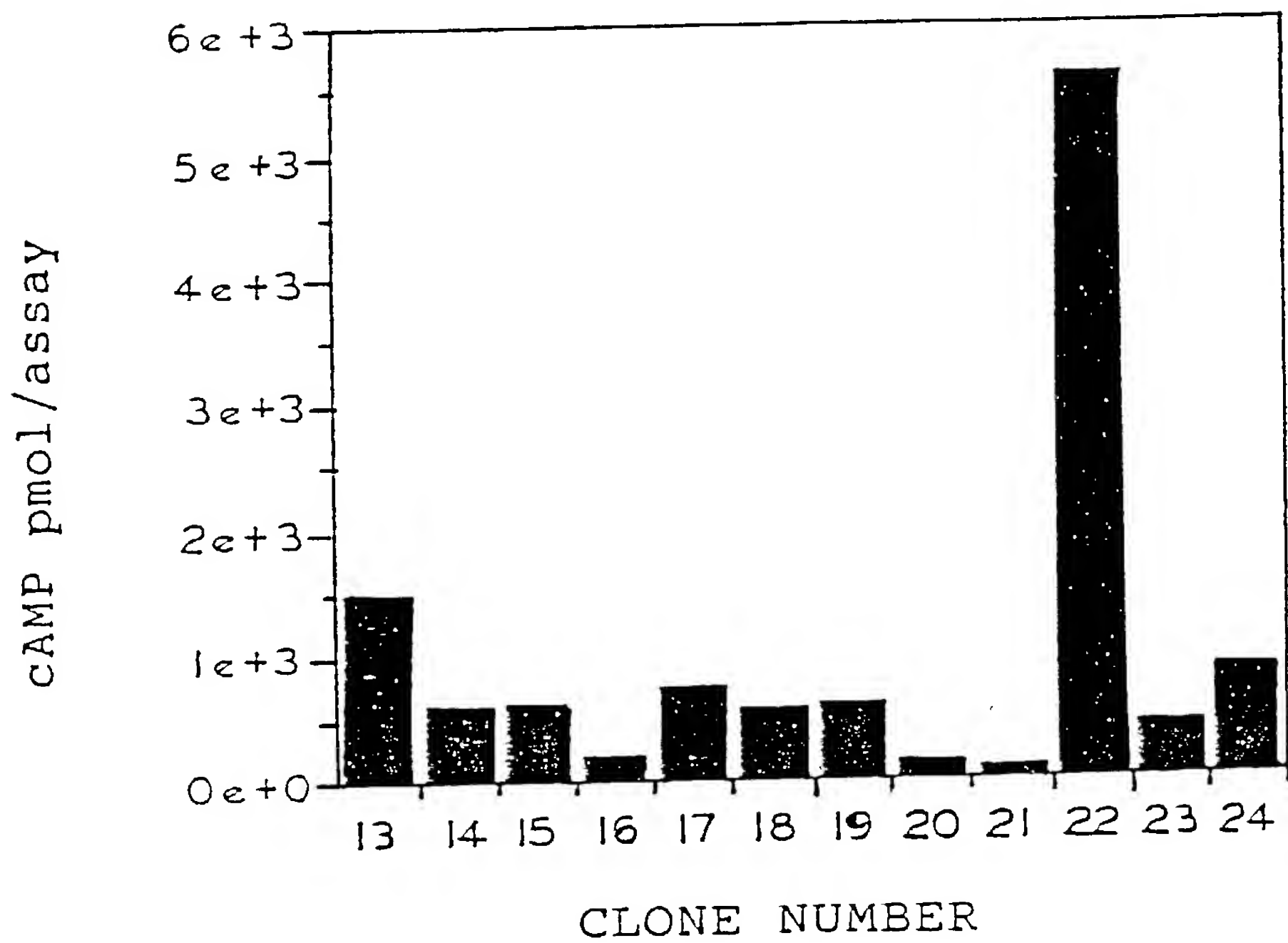
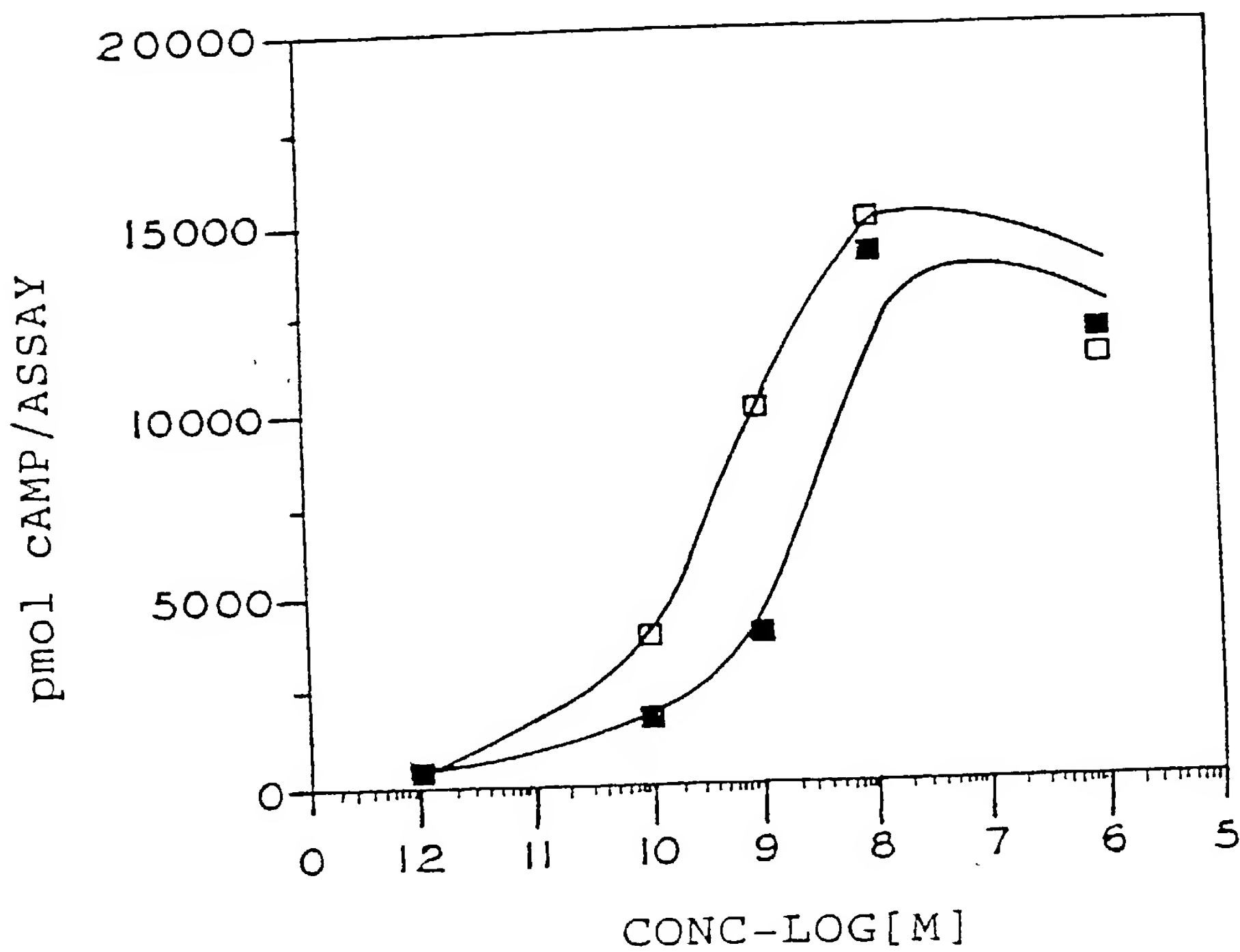


FIG. 7

EFFECT OF CGRP8-37 ON CGRP-MEDIATED
cAMP IN pCDNHCGRP α STABLY
TRANSFORMED 293 CELLS (CLONE 22)



□ CGRP
■ CGRP 8-37 (100nM)

[125I]CGRP BINDING TO pCDNHCGPr TRANSFORMED
293 CELLS (CLONE 22) MEMBRANES

FIG. 8A

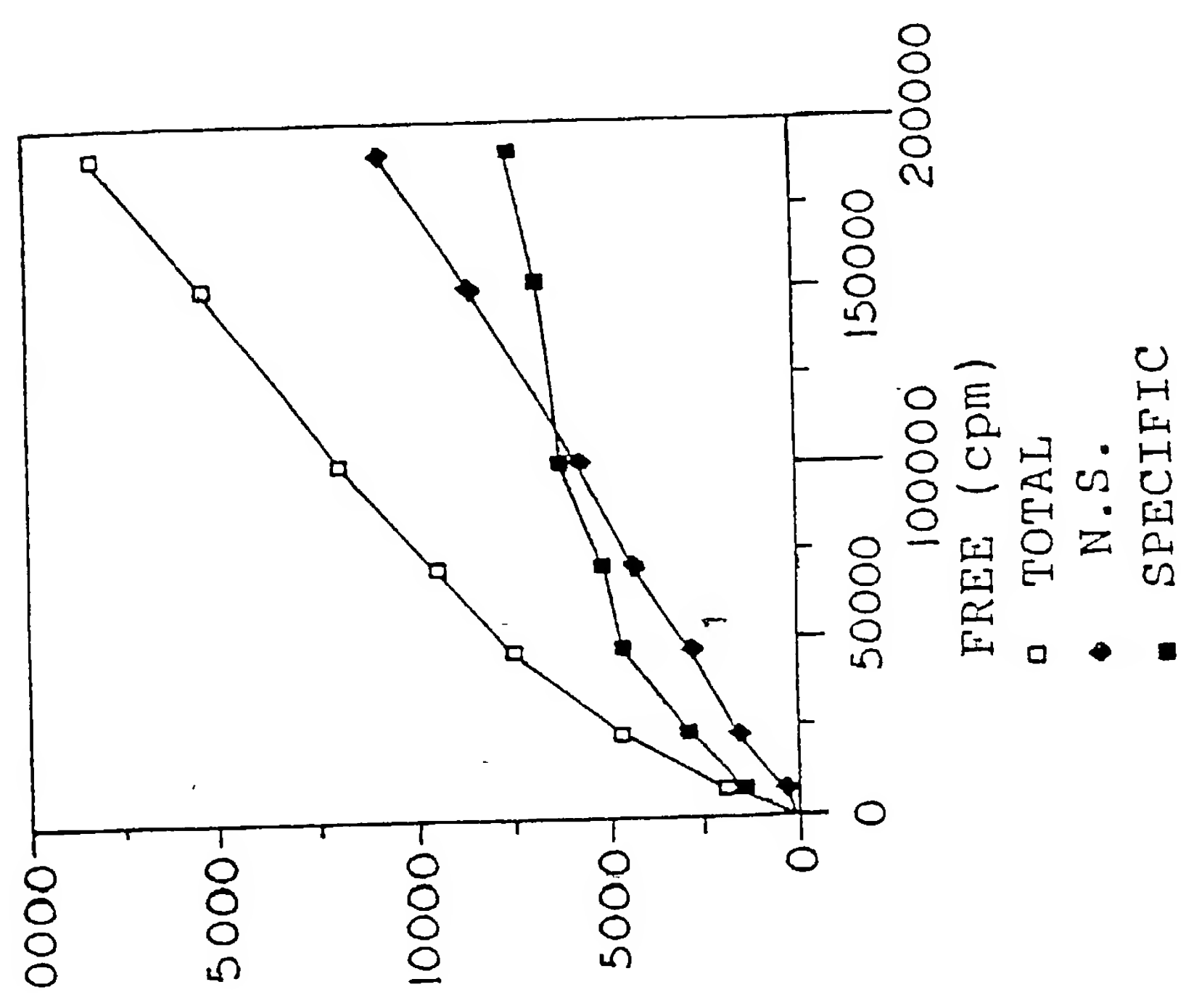


FIG. 8B

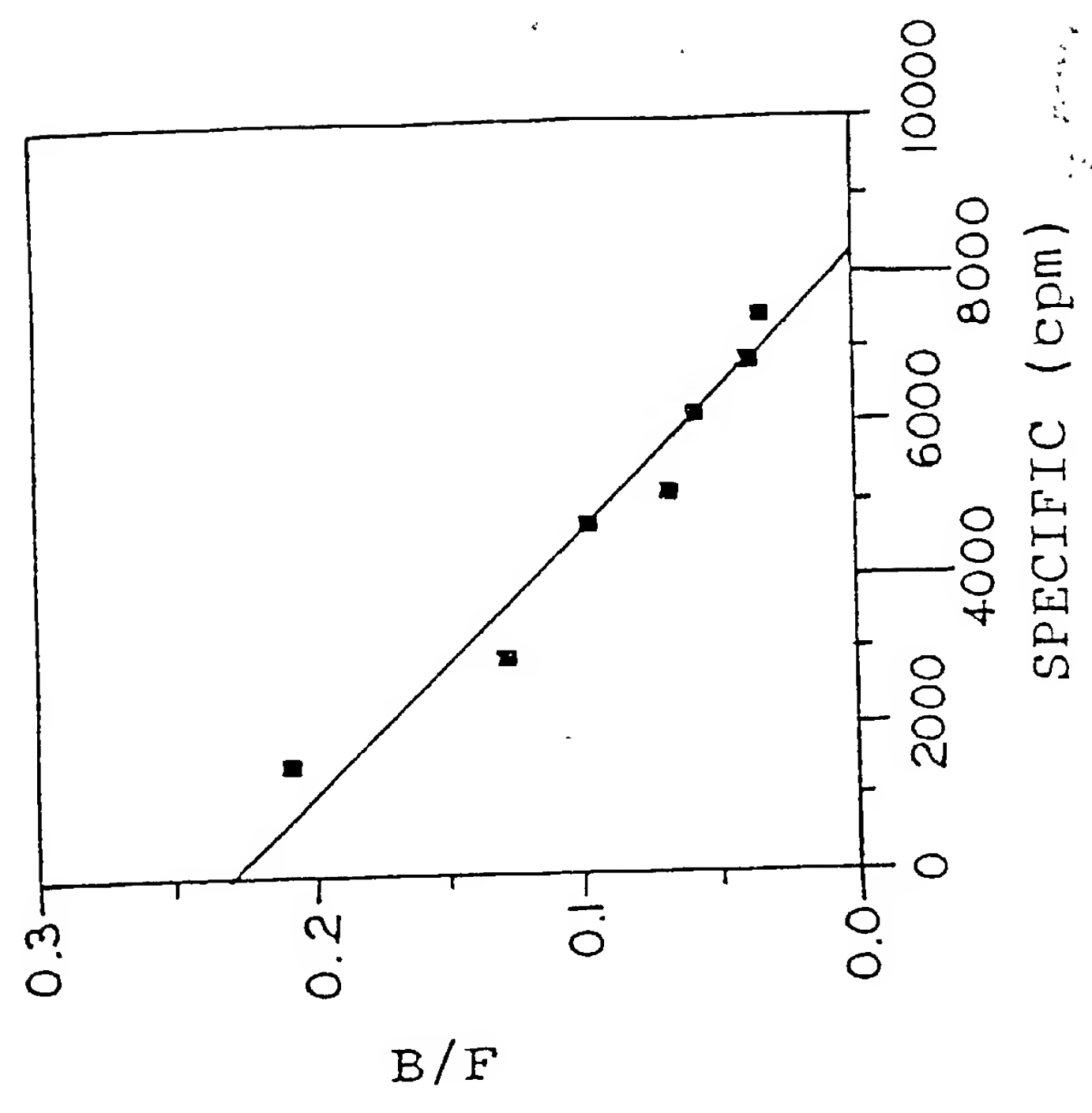
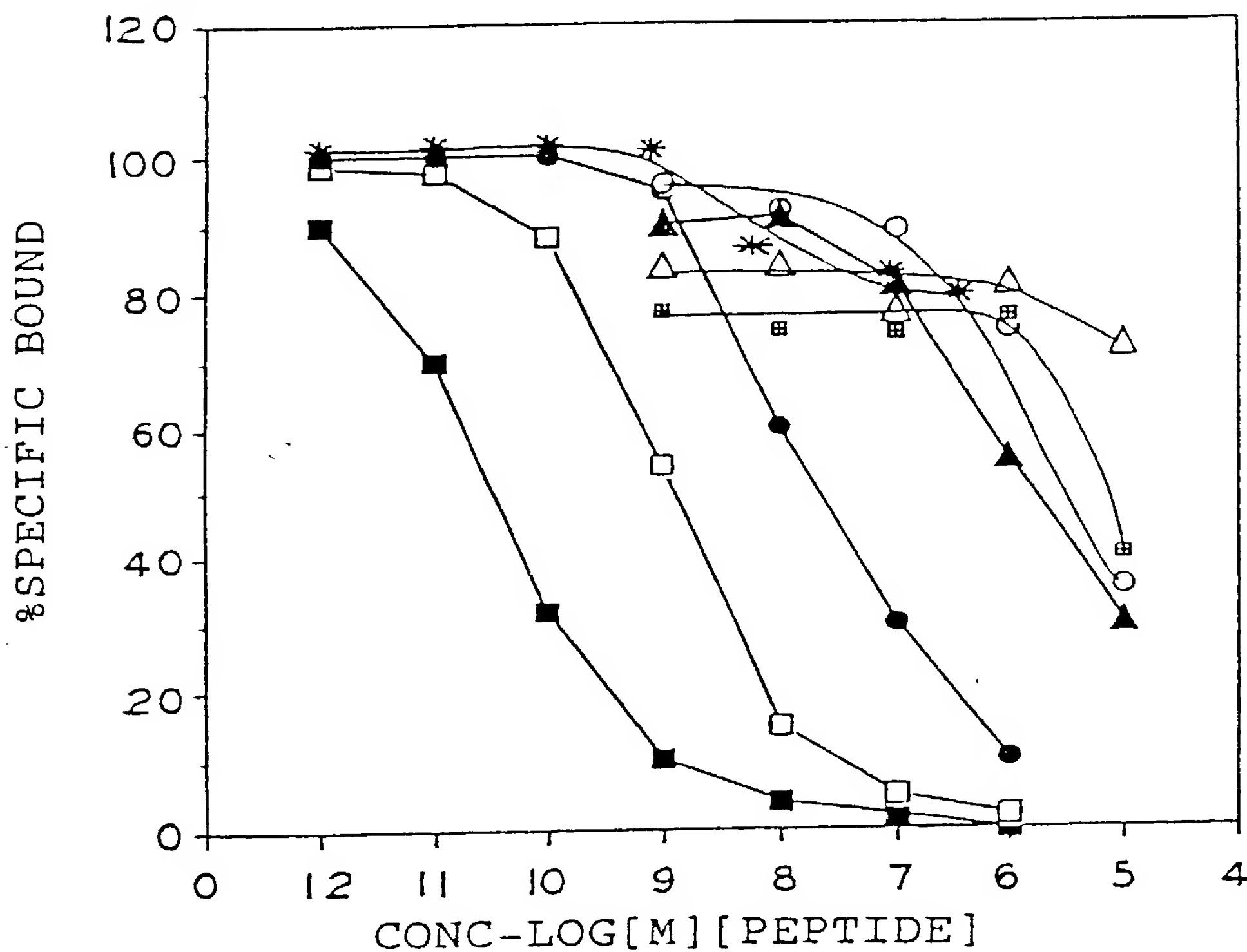
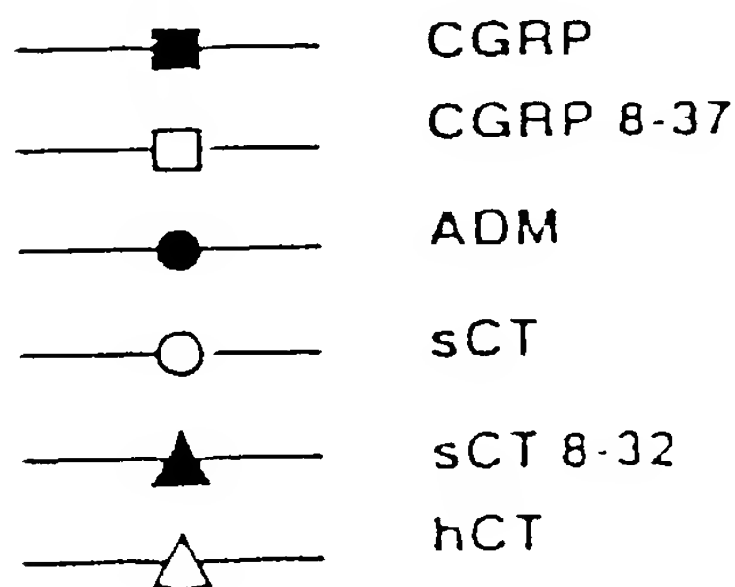


FIG. 9

COMPETITION CURVES FOR
REPRESENTATIVE CGRP ANALOGS AGAINST
[125I]CGRP BINDING IN pCDNHCGRP α
TRANSFORMED CELL (CLONE22) MEMBRANES



CGRP > CGRP 8-37 > ADM > sCT 8-32 > sCT > VIP > Amylin, LCT



Comparison of Human CGRP and Human Calcitonin Receptor Amino Acid Sequences

FIG. 10A

```

1  ....MEKKCTLYFLVL...LPFFMILVTAELEESPEDSIQLGVTRNKIMT 43
      . . . | . | . | . | . | . | . | . | . | . | . | . | . |
      . . . . | . | . | . | . | . | . | . | . | . | . | . | . |
1 MRFTFTRCLALFLLNHPTPILPAFSNQTYPTIEPKPFLYVVGRKKMMD 50

44 AQYECYQKINQDPIQQAEGVYCNRTWDGWLWCVNDVAAGTESMQLCPDYFQ 93
      ||||| : : : | | : ||| ||||| : : ||| | : |||||
51 AQYKCYDRNQQLPAYQGEQGYCNRTWDGWLWCVNDVPTAGVLSYQFCPDYFP 100

94 DFDPSEKVTKICDQDGNWFRHPASNRTWTNYTQCNVNTHEKVKTALNLFY 143
      ||||| ||||| : : : | ||||| : : ||| ||| : : ||| : : |
101 DFDPSEKVTKYCDEKGVWFKHPENNRRTWSNYTMCNAFTPEKLKNAYVLYY 150

144 LTIIGHGLSIASLLISLGIFFFYFK.....SLSCQRITLH 177
      | : ||| : ||| | : ||||| : : | : ||||| : |||
151 LAIVGHSLSIFTLVISLGIFVFFERKLTTFPLNWKYRKALSLGCQRVTLH 200
      -----|-----
178 KNLFFSFVCNSVVTIIHLTAVANNQALVATNPVSCKVSQFIHLYLNGCNY 227
      MATCH WITH FIG. 10B

```

30031103 033102

FIG. 10B

MATCH WITH FIG. 10A

201 KNMFLTYILNSMIIIIHLVEVPNGELVRRDPVSKILHFFHQYMMACNY 250
 228 FWMLCEGIYLTIVVAVFAEKQHLMWYYFLGWGFPLIPACIHAIARSLY 277
 251 FWMLCEGIYLTIVVAVFTEKQRLRWYYLLGWGFPLVPTTIHAITRAVY 300
 278 YDNCWISSDTHLLYIIHGPICAALLVNLFLLNIVRVLITKLVTHQAE 327
 301 FNDNCWLSVETHLLYIIHGPVMAALVNVFFLLNIVRVLVTKMRETHEAE 350
 328 SNLYMKAVRATLILVPLLGIIEFVLIPWRPEGKIAEEVDYIMHILMHFQG 377
 351 SHMYLKAVKATMILVPLLGIQFVVFPWRPSNKMMLGKIYDYVMHSLIHFQG 400
 378 LLVSTIFCFFNGEVQAILRRNWNQYKIQFGNSFSNSEALRSASYTVSTIS 427
 401 FFVATIYCFNCNNEVQTTVKRQWAQFKIQWNQRWGRRPSNRSARAAAAAAE 450
 428 DGPGYSHDCPSEHLNGKS.IHDIENVLLKPENLYN..... 461
 451 AGDIPIYICHQEPNRPANNQGEESAIEIPLNIEQESSA 490

10051486, 093102

Comparison of Human and Rat CGRP Receptor Amino Acid Sequences

MATCH WITH FIG. 11B

Detailed description of Figure 6: This is a scatter plot titled 'The relationship between fertility and literacy'. The vertical axis (y-axis) is labeled 'Number of children per woman at birth' and has major tick marks at 0, 2, 4, 6, and 8. The horizontal axis (x-axis) is labeled 'Percentage of women who are literate' and has major tick marks at 0, 20, 40, 60, 80, and 100. There are approximately 15 data points scattered across the plot. Most points are clustered in the upper-left quadrant (high fertility, low literacy), indicating that in many developing countries, women have many children despite having low literacy levels. As literacy increases towards the right side of the graph, the number of children per woman generally decreases, moving points towards the lower-right quadrant.

FIG. 11B

MATCH WITH FIG. 11A

250 QHLMWYFLGWGFLLPACIHAIARSLYNDNCWISSDTHLLYIIHGPI 299
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 250 QHLMWYFLGWGFLLPACIHAIARSLYNDNCWISSDTHLLYIIHGPI 299
 -----IV-----
 300 AALLVNLFLLNIVRLITKLKVTHQAESNLYMKAVRATLILVPLLGIEF 349
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 300 AALLVNLFLLNIVRLITKLKVTHQAESNLYMKAVRATLILVPLLGIEF 349
 -----V-----VI-----
 350 VLIWRPECKIAEEVDYIMHILMHFQGLLVSTIFCFNGEVQAILRRNW 399
 ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 350 VLIWRPECKIAEEVDYIMHILMHFQGLLVSTIFCFNGEVQAILRRNW 399
 -----VII-----
 400 NQYKIQFGNSFNSEALRSASYTVSTISDCGPGYSHDCPSEHLNGKSIHDI 449
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 400 NQYKIQFGNSFNSEALRSASYTVSTISDCGPGYSHDCPSEHLNGKSIHDI 449

 450 ENVLLKPENLYN... 461
 ||| ||||:|:
 450 ENVALKPEKMYDLVM 464

10034100 003400

